

AMENDMENTS TO THE SPECIFICATION:

Please replace the paragraph beginning at page 8, line 19, with the following rewritten paragraph:

A preferred nucleotide sequence for a *Rht* gene is one which encodes the RHT amino acid sequence shown in Figure 3b, especially a *Rht* coding sequence shown in Figure 3a. A preferred *rht* mutant lacks part or all of the 17 amino acid sequence underlined in Figure 3b, and/or part or the sequence DVAQKLEQLE (SEQ ID NO:4), which immediately follows the 17 amino acid sequence underlined in Figure 3b.

Please replace the paragraph beginning at page 17, line 1, with the following rewritten paragraph:

The present invention also extends to nucleic acid encoding *Rht* or a homologue obtainable using a nucleotide sequence derived from Figure 2 or Figure 3a, and such nucleic acid obtainable using one or more, e.g. a pair, of primers including a sequence shown in Table 1 (SEQ ID NO:21-SEQ ID NO:55).

Please replace the paragraph beginning at page 18,
line 13, with the following rewritten paragraph:

Some preferred embodiments of polypeptides according to the present invention (encoded by nucleic acid embodiments according to the present invention) include the 17 amino acid sequence which is underlined in Figure 3b, or a contiguous sequence of amino acids residues with at least about 10 residues with similarity or identity with the respective corresponding residue (in terms of position) in 17 amino acids which are underlined in Figure 3b, more preferably 11, 12, 13, 14, 15, 16 or 17 such residues, and/or the sequence DVAQKLEQLE, or a contiguous sequence of amino acids with at least about 5 residues with similarity or identity with the respective corresponding residue (in terms of position) within DVAQKLEQLE, more preferably 6, 7, 8 or 9 such residues. Further embodiments include the 27 amino acid sequence DELLAALGYKVRASDMADVAQKLEQLE (SEQ ID NO:56), or a contiguous sequence of amino acids residues with at least about 15 residues with similarity or identity with the respective corresponding residue (in terms of position) within this sequence, more preferably 16, 17, 18, 19, 20, 21, 22, 23, 24, 25 or 26 such residues.

Please replace the paragraph beginning at page 19, line 6, with the following rewritten paragraph:

As is well-understood, homology at the amino acid level is generally in terms of amino acid similarity or identity. Similarity allows for "conservative variation", i.e. substitution of one hydrophobic residue such as isoleucine, valine, leucine or methionine for another, or the substitution of one polar residue for another, such as arginine for lysine, glutamic for aspartic acid, or glutamine for asparagine. Similarity may be as defined and determined by the TBLASTN program, of Altschul et al. (1990) J. Mol. Biol. 215: 403-10, which is in standard use in the art, or more preferably GAP (Program Manual for the Wisconsin Package, Version 8, September 1994, Genetics Computer Group, 575 Science Drive, Madison, USA), which uses the algorithm of Needleman and Wunsch to align sequences. Suitable parameters for GAP include the default parameters, a gap creation penalty = 12 and gap extension penalty = 4, or gap creation penalty 3.00 and gap extension penalty 0.1. Homology may be over the full-length of the Rht sequence of Figure 3b, or may more preferably be over a contiguous sequence of 10 amino acids compared with

DVAQKLEQLE (SEQ ID NO:4), and/or a contiguous sequence of 17 amino acids, compared with the 17 amino acids underlined in Figure 3b, and/or a contiguous sequence of 27 amino acids compared with DELLAALGYKVRASDMADVAQKLEQLE (SEQ ID NO:56), or a longer sequence, e.g. about 30, 40, 50 or more amino acids, compared with the amino acid sequence of Figure 3b and preferably including the underlined 17 amino acids and/or DVAQKLEQLE (SEQ ID NO:4).

Please replace the paragraph beginning at page 20, line 6, with the following rewritten paragraph:

At the nucleic acid level, homology may be over the full-length or more preferably by comparison with the 30 nucleotide coding sequence within the sequence of Figure 3a and encoding the sequence DVAQKLEQLE (SEQ ID NO:4) and/or the 51 nucleotide coding sequence within the sequence of Figure 3a and encoding the 17 amino acid sequence underlined in Figure 3b, or a longer sequence, e.g. about, 60, 70, 80, 90, 100, 120, 150 or more nucleotides and preferably including the 51 nucleotide of Figure 3 which encodes the underlined 17 amino acid sequence of Figure 3b.

Please replace the paragraph beginning at page 25, line 8, with the following rewritten paragraph:

If need be, stringency can be increased by increasing the temperature of the washes, and/or reducing or even omitting altogether, the SSC in the wash solution.

Please replace the paragraph beginning at page 25, line 16, with the following rewritten paragraph:

Homologues to rht mutants are also provided by the present invention. These may be mutants where the wild-type includes the 17 amino acids underlined in Figure 3b, or a contiguous sequence of 17 amino acids with at least about 10 (more preferably 11, 12, 13, 14, 15, 16 or 17) which have similarity or identity with the corresponding residue in the 17 amino acid sequence underlined in Figure 3, but the mutant does not. Similarly, such mutants may be where the wild-type includes DVAQKLEQLE or a contiguous sequence of 10 amino acids with at least about 5 (more preferably 6, 7, 8 or 9) which have similarity or identity with the corresponding residue in the sequence DVAQKLEQLE, but the mutant does not. Nucleic acid encoding such mutant polypeptides may on expression in a plant confer a

phenotype which is insensitive or unresponsive to treatment of the plant with GA, that is a mutant phenotype which is not overcome or there is no reversion to wild-type phenotype on treatment of the plant with GA (though there may be some response in the plant on provision or depletion of GA) .

Page 41, before the paragraph beginning at line 23, insert the following new heading:

Brief Description of the Drawings

Please replace the paragraph beginning at page 41, line 25, with the following rewritten paragraph:

Figure 1: Alignment of N-terminus predicted GAI amino acid sequence (Gai) (SEQ ID NO:78) with rice EST D39460 (0830) (SEQ ID NO:79), with a region of homology outlined in black.

Please replace the paragraph beginning at page 42, line 1, with the following rewritten paragraph:

Figures 2a-2c. DNA sequences from C15-1, 14a1 and 5a1:

Please replace the paragraph beginning at page 42,
line 3, with the following rewritten paragraph:

Figure 2a shows a consensus DNA sequence cDNA C15-1
(obtained via single-pass sequencing) (SEQ ID NO:57).

Please replace the paragraph beginning at page 42,
line 6, with the following rewritten paragraph:

Figure 2b shows data from original DNA sequencing runs
from 14a1 (single-pass) (SEQ ID NO:58-SEQ ID NO:70).

Please replace the paragraph beginning at page 42,
line 9, with the following rewritten paragraph:

Figure 2c shows data from original DNA sequencing runs
from 5a1 (single-pass) (SEQ ID NO:71-SEQ ID NO:77).

Please replace the paragraph beginning at page 42,
line 12, with the following rewritten paragraph:

Figures 3a and 3b. Rht sequences:

Please replace the paragraph beginning at page 42,
line 14, with the following rewritten paragraph:

Figure 3a shows a composite DNA sequence of wheat *Rht* gene derived from data in Figure 2, including coding sequence (SEQ ID NO:3).

Please replace the paragraph beginning at page 42, line 17, with the following rewritten paragraph:

Figure 3b shows an alignment of the entire predicted *Rht* protein sequence encoded by the coding sequence of Figure 2 (*rht*) with the entire predicted *GAI* protein sequence of *Arabidopsis* (*Gai*) (SEQ ID NO:1 and SEQ ID NO:2). Regions of sequence identity are highlighted in black.

Please replace the paragraph beginning at page 42, line 23, with the following rewritten paragraph:

Figures 4a and 4b. D39460 sequence:

Please replace the paragraph beginning at page 42, line 25, with the following rewritten paragraph:

Figure 4a shows DNA sequence (single-pass) of rice cDNA D39460 (SEQ ID NO:19). This cDNA is an incomplete,

partial clone, missing the 3' end of the mRNA from which it is derived.

Please replace the paragraph beginning at page 43, line 1, with the following rewritten paragraph:

Figure 4b shows alignment of the entire predicted Rht protein sequence (wheat - encoded by the coding sequence of Figure 2) with that of GAI (Gai) and rice protein sequence predicted from DNA sequence in Figure 4a (Rice) (SEQ ID NO:20). Regions of amino acid identity are highlighted in black; some conservative substitutions are shaded.

Please replace the paragraph beginning at page 43, line 10, with the following rewritten paragraph:

Figures 6a and 6b. Rice EST sequence:

Please replace the paragraph beginning at page 43, line 12, with the following rewritten paragraph:

Figure 6a shows the nucleotide sequence of rice EST D39460, as determined by the present inventors (SEQ ID NO:12).

Please replace the paragraph beginning at page 43,
line 15, with the following rewritten paragraph:

Figure 6b shows the predicted amino acid sequence (SEQ
ID NO:5) encoded by the rice EST sequence of Figure 6a.

Please replace the paragraph beginning at page 43,
line 18, with the following rewritten paragraph:

Figures 7a and 7b. Wheat C15-1 cDNA:

Please replace the paragraph beginning at page 43,
line 20, with the following rewritten paragraph:

Figure 7a shows the nucleotide sequence of the wheat
C15-1 cDNA (SEQ ID NO:13).

Please replace the paragraph beginning at page 43,
line 23, with the following rewritten paragraph:

Figure 7b shows the predicted amino acid sequence (SEQ
ID NO:6) of the wheat C15-1 cDNA of Figure 7a.

Please replace the paragraph beginning at page 43,
line 26, with the following rewritten paragraph:

Figures 8a and 8b. Wheat 5a1 genomic clone:

Please replace the paragraph beginning at page 43,
line 28, with the following rewritten paragraph:

Figure 8a shows the nucleotide sequence of the 5a1
wheat genomic clone (SEQ ID NO:14).

Please replace the paragraph beginning at page 44,
line 3, with the following rewritten paragraph:

Figure 8b shows the predicted amino acid sequence (SEQ
ID NO:7) of the 5a1 wheat genomic clone of Figure 8a.

Please replace the paragraph beginning at page 44,
line 6, with the following rewritten paragraph:

Figures 9a and 9b. Maize 1a1 genomic clone:

Please replace the paragraph beginning at page 44,
line 8, with the following rewritten paragraph:

Figure 9a shows the nucleotide sequence of the 1a1
maize genomic clone, i.e. D8 (SEQ ID NO:15).

Please replace the paragraph beginning at page 44,
line 11, with the following rewritten paragraph:

Figure 9b shows the amino acid sequence (SEQ ID NO:8)
of the maize 1a1 genomic clone of Figure 9a.

Please replace the paragraph beginning at page 44,
line 19, with the following rewritten paragraph:

Figures 11a-11d. Sequences of maize D8 alleles:

Please replace the paragraph beginning at page 44,
line 21, with the following rewritten paragraph:

Figure 11a shows a partial nucleotide sequence of the
maize D8-1 allele (SEQ ID NO:16).

Please replace the paragraph beginning at page 44,
line 24, with the following rewritten paragraph:

Figure 11b shows a partial amino acid sequence (SEQ ID
NO:9) of the maize D8-1 allele.

Please replace the paragraph beginning at page 44,
line 27, with the following rewritten paragraph:

Figure 11c shows a partial nucleotide sequence of the
maize D8-2023 allele (SEQ ID NO:17).

Please replace the paragraph beginning at page 45,
line 1, with the following rewritten paragraph:

Figure 11d shows a partial amino acid sequence (SEQ ID
NO:10) of the maize D8-2023 allele.

Please replace the paragraph beginning at page 45,
line 4, with the following rewritten paragraph:

Figures 12a and 12b. Wheat *rht-10* allele:

Please replace the paragraph beginning at page 45,
line 6, with the following rewritten paragraph:

Figure 12a shows a partial nucleotide sequence of the
wheat *rht-10* allele (SEQ ID NO:18).

Please replace the paragraph beginning at page 45,
line 9, with the following rewritten paragraph:

Figure 12b shows a partial amino acid sequence (SEQ ID NO:11) of the wheat *rht-10* allele.

Please replace the paragraph beginning at page 45, line 23, with the following rewritten paragraph:

Previously, we cloned the *GAI* gene of *Arabidopsis* (PCT/GB97/00390 - WO97/29123 published 14 August 1997). Comparison of the DNA sequences of the wild-type (*GAI*) and mutant (*gai*) alleles showed that *gai* encodes a mutant predicted protein product (*gai*) which lacks a segment of 17 amino acids from close to the N-terminus of the protein. Screening of the DNA sequence databases with the *GAI* sequence revealed the existence of a rice EST (D39460) which contains a region of sequence very closely related to that of the segment that is deleted from *GAI* in the *gai* protein. A comparison of the predicted amino acid sequences from the region DELLA (SEQ ID NO:107) to EQLE (SEQ ID NO:108) are identical in both sequences. The two differences (V/A; E/D) are conservative substitutions, in which one amino acid residue is replaced by another having very similar chemical properties. In addition, the region of identity extends beyond the boundary of the deletion

region in the gai protein. The sequence DVAQKLEQLE is not affected by the deletion in gai, and yet is perfectly conserved between the GAI and D39460 sequences (Figure 1).

Please replace the paragraph beginning at page 47, line 3, with the following rewritten paragraph:

Figure 2a gives the complete (single-pass) DNA sequence of cDNA C15-1. We have also obtained DNA sequence for C15-10; it is identical with that of C15-1, and is therefore not shown. Figures 2b and 2c show original data from individual sequencing runs from clones 14a1 and 5a1. The sequences shown in Figure 2 can be overlapped to make a composite DNA sequence, shown in Figure 3a. This sequence displays strong homology with that of Arabidopsis GAI, as revealed by a comparison of the amino acid sequence of a predicted translational product of the wheat sequence (Rht) with that of GAI (GAI), shown in Figure 3b. In particular, the predicted amino acid sequence of the presumptive Rht reveals a region of near-identity with GAI over the region that is missing in gai (Figure 4). Figure 4 reveals that the homology that extends beyond the gai deletion region in the rice EST is also conserved in Rht (DVAQKLEQLE (SEQ ID

NO:4)), thus indicating that this region, in addition to that found in the *gai* deletion, is involved in GA signal-transduction. This region is not found in SCR, another protein that is related in sequence to GAI but which is not involved in GA signalling. The primers used in the above sequencing experiments are shown in Table 1.

Please replace the paragraph beginning at page 49, line 20, with the following rewritten paragraph:

Mutations were found in the candidate *D8* and *Rht* genes in each of the above mutants. The *D8*-1 mutation is an in-frame deletion which removes amino acids VAQK (SEQ ID NO:101) (55-59) and adds a G (see sequence in Figure 11a and Figure 11b). This deletion overlaps with the conserved DVAQKLEQLE homology block described above. *D8*-2023 is another in-frame deletion mutation that removes amino acids LATDTVHYNPSD (SEQ ID NO:102) (87-98) from the N-terminus of the *D8* protein (see Figure 11c and Figure 11d). This deletion does not overlap with the deletion in *gai* or *D8*-1, but covers another region that is highly conserved between GAI, *D8* and *Rht* (see Figure 10). Finally, *Rht*-*D1c* contains another small in-frame deletion that removes amino acids LNAPPPPLPPAPQ (SEQ ID NO:103) (109-121) in the N-terminal

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region of the mutant Rht protein that it encodes (see Figure 12a and Figure 12b) (LN-P is conserved between GAI, D8 and Rht, see Figure 10).

Please replace the paragraph beginning at page 52, line 1, with the following rewritten paragraph:

TABLE 2 - Primers used in the sequence of D-8 clones (SEQ ID NO:80-SEQ ID NO:100)

Before the figures, insert the Sequence Listing submitted herewith on separate sheets.